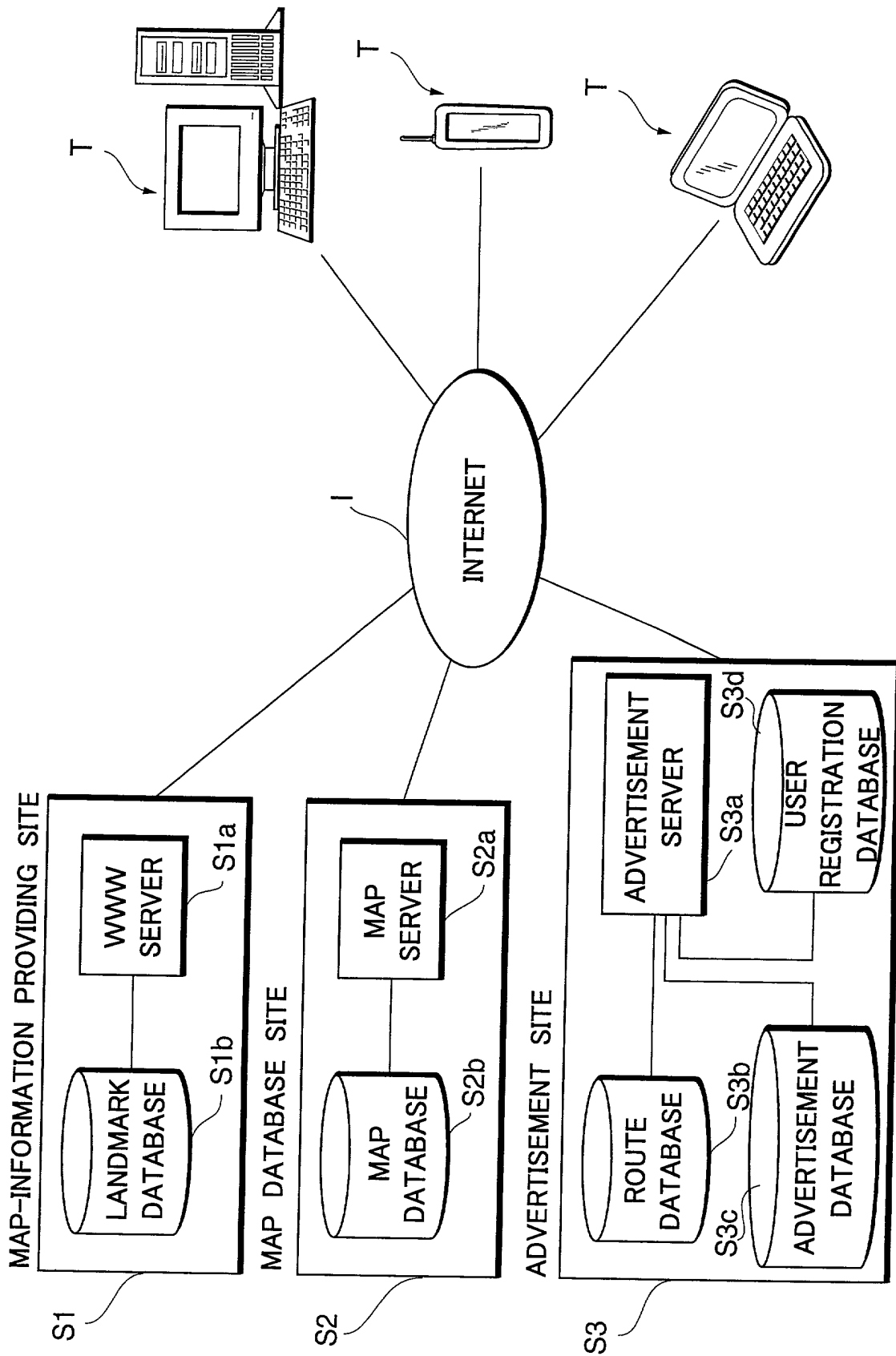


FIG.1



1. *Phylogenetic relationships* – The phylogenetic relationships among the 10 species of *Phrynosoma* were inferred using a Bayesian approach. The analysis was performed using the software package MrBayes 3.2.2 (Ronquist & Huelsenbeck 2003). The nucleotide substitution model was selected using jModelTest 2.1.10 (Darriba et al. 2012). The analysis was run for 10 000 000 generations, with a burn-in of 10 000 000 generations. The posterior probability of the tree was calculated using the software package Tracer 1.7.1 (Rambaut 2016).



FIG.3

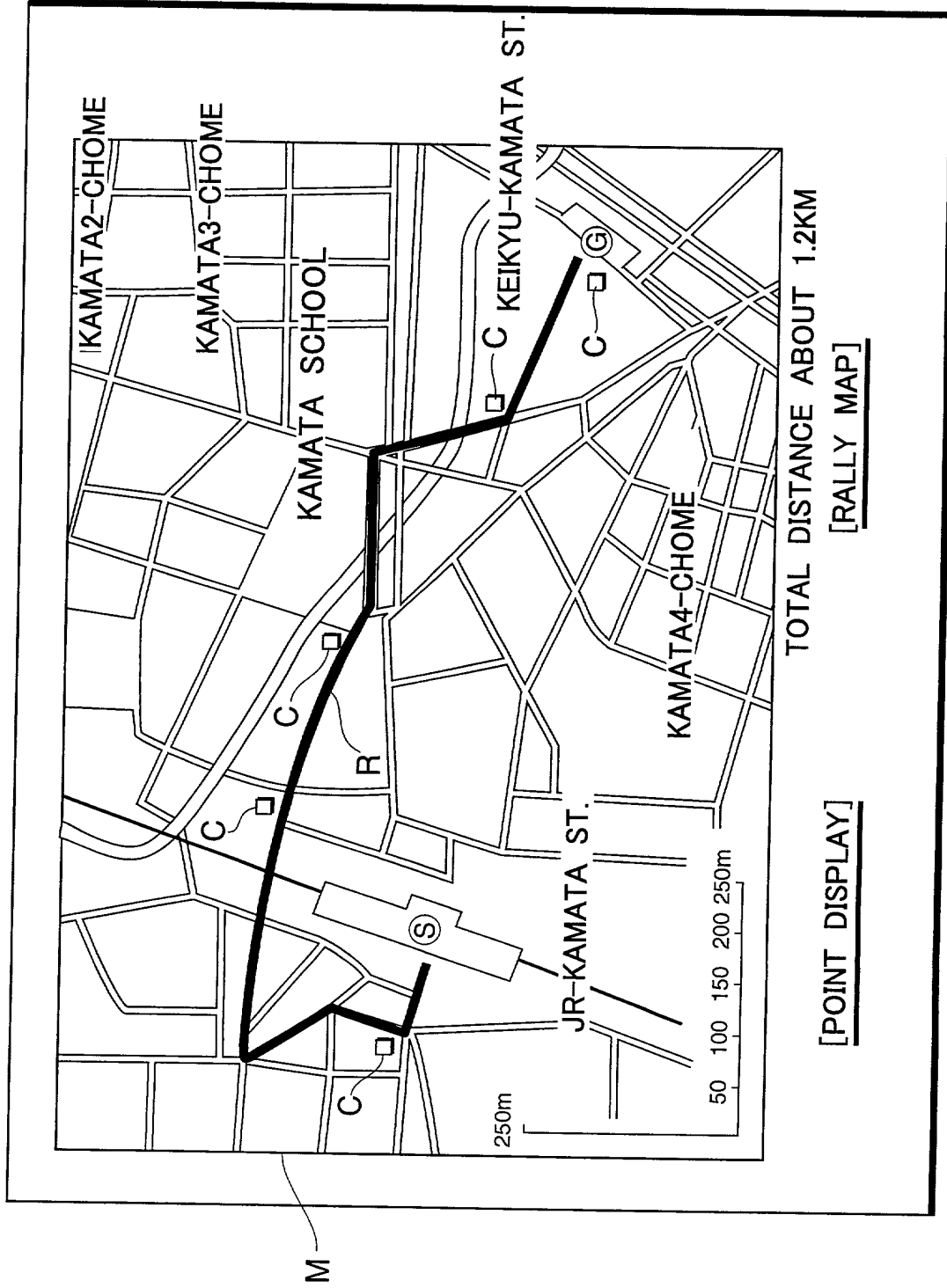


FIG.4

PRIOR ART

